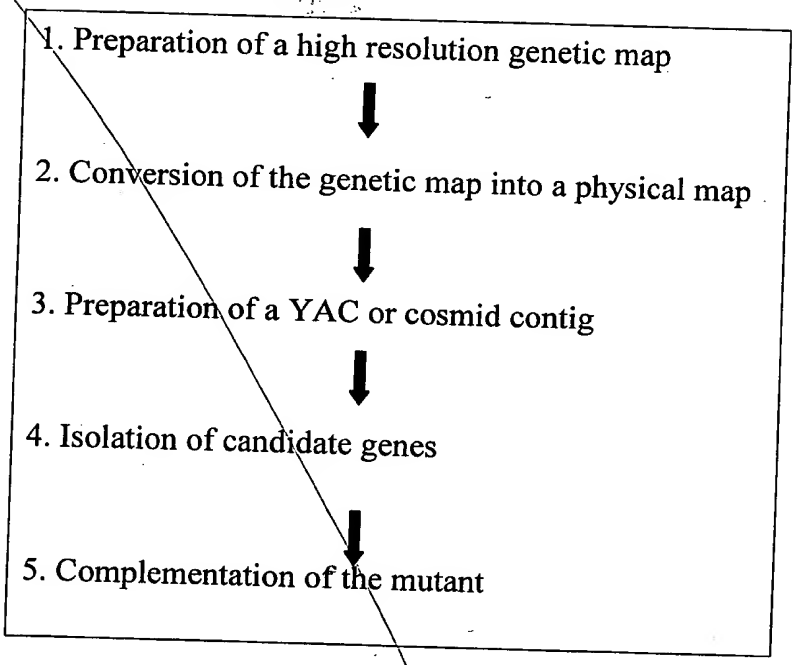
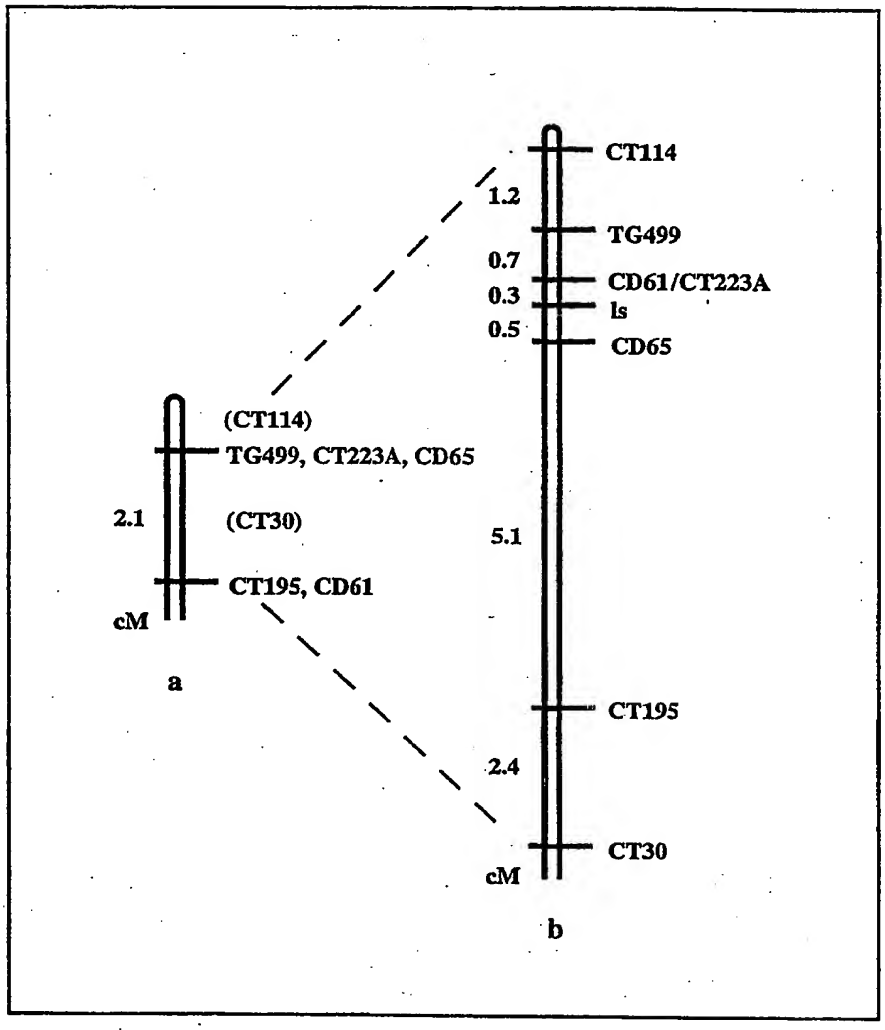


Fig. 1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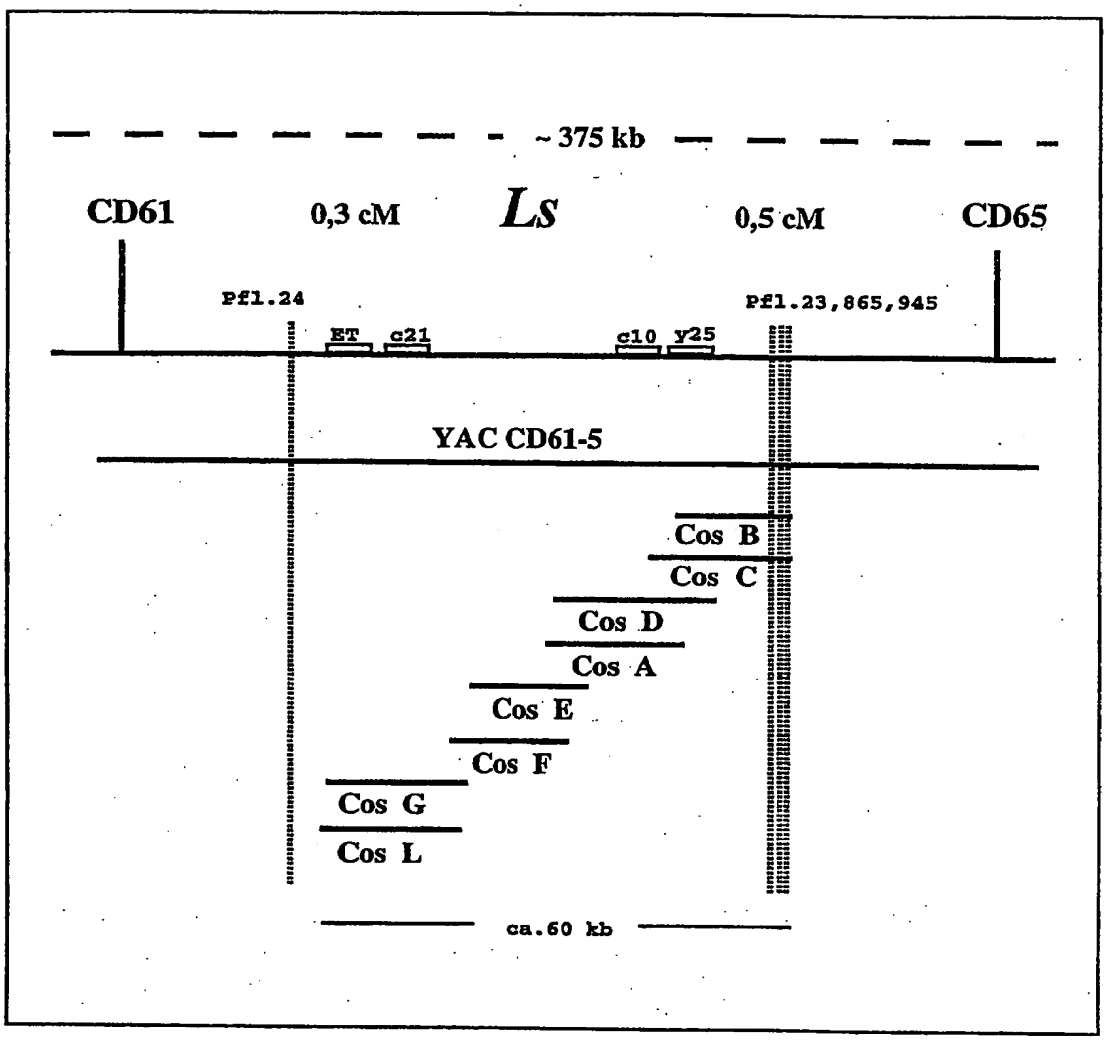
TG499
0.7
CD61/CT223A
0.3
ls
0.5
CD65
(CT114)
TG499, CT223A, CD65
2.1
(CT30)
5.1
CT195, CD61
cM
a
CT195
2.4
CT30
cM
b

Fig. 2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Cos B
Cos C
Cos D
Cos A
Cos E
Cos F
Cos G
Cos L
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Fig. 3

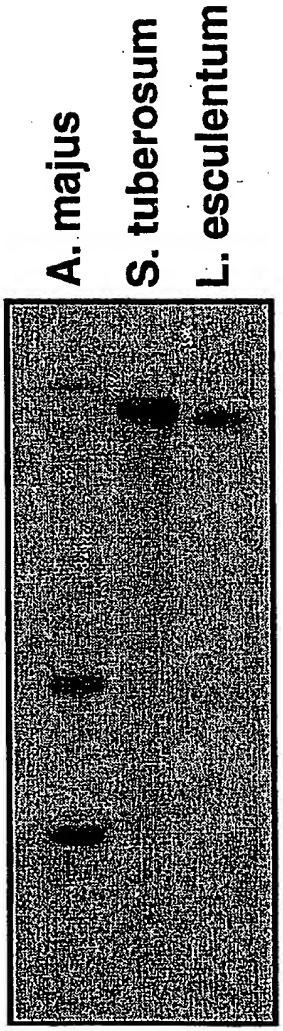

Fig. 4

```
      E  A  N  H  N  H  P  L  F  L  Q  R  F  I  E  A  L  D  Y  Y
1081  TACAGCTGTGTTTGATTCACTGGAAGCTACATTGCCACCGGGTAGTCGAGAGAGGATGAC  1140
      T  A  V  F  D  S  L  E  A  T  L  P  P  G  S  R  E  R  M  T
1141  AGTTGAACAAGTGTGGTTTGGGAGAGAGATTGTTGATATCGTTGCGATGGAAGGAGATAA  1200
      V  E  Q  V  W  F  G  R  E  I  V  D  I  V  A  M  E  G  D  K
1201  AAGGAAAGAAAGACATGAAAGGTTTAGATCATGGGAAGTTATGTTGAGGAGTTGTGGATT  1260
      R  K  E  R  H  E  R  F  R  S  W  E  V  M  L  R  S  C  G  F
1261  TAGTAATGTTGCTTTAAGCCCTTTTGCATTATCACAAGCTAAGCTTCTTTTGAGACTTCA  1320
      S  N  V  A  L  S  P  F  A  L  S  Q  A  K  L  L  L  R  L  H
1321  TTATCCTTCTGAAGGCTATCAACTCGGAGTTTCGAGTAATTCTTTCTTCTTAGGTTGGCA  1380
      Y  P  S  E  G  Y  Q  L  G  V  S  S  N  S  F  F  L  G  W  Q
1381  AAATCAACCCCTTTTCTCCATCTCGTCTTGGCGTTGAGAAAAACTATCAAATAGCCAACT  1440
      N  Q  P  L  F  S  I  S  S  W  R
1441  TCAGAGGGTAATTAAGACTACTGATAGTTTAGGAGGGATCTGAAGAAAACGCGTGGAGTG  1500

1501  AAAACCCTAAATAACCAGATTTTCTAATGAAGTTGTAGTAGTAGAAATTTGCATGGTGAA  1560

1561  GAACAATATTGAAGAGGTATTGAAATTTCATGTTTTTTTTGTTTTACTTATTGATATGAA  1620

1621  TGTTTTAAAATTTTTAACATAGAGGACTAGGTTGATGATATATAGTATTTAAGTTAACTA  1680

1681  GTCTTTGTATAACGCAAGATCTTGATCAACTTATTTTTATTTTTAATTA  1729
```

Fig. 5

```
1    CCTCTGTCCTTCCCCCCAGGTCCCCTTTTTTTCCTTTCTCTCTCTCCTTTATTTCTCTTT   60

61   TCATAAGCATATTCTTTCTCTCTCTAGGGTTTTCACTTTCACCTGAAATAGTGTTGTTAA  120

121  ATTGAATGATATGTTAGGATCCTTTGGTTCTTCATCATCTCAATCTCACCCTCATCATGA  180
                M  L  G  S  F  G  S  S  S  S  Q  S  H  P  H  H  D

181  TGAAGAATCTTCTGATCATCATCAACAGCGTAGATTCACCGCTACTGCTACAACTATCAC  240
      E  E  S  S  D  H  H  Q  Q  R  R  F  T  A  T  A  T  T  I  T

241  CACCACCACCATCACTACCTCACCAGCTATTCAAATCCGCCAGCTACTCATTAGCTGTGC  300
      T  T  T  I  T  T  S  P  A  I  Q  I  R  Q  L  L  I  S  C  A

301  GGAGTTGATTTCGCAGTCCGATTTCTCGGCCGCGAAAAGACTCCTTACTATATTATCAAC  360
      E  L  I  S  Q  S  D  F  S  A  A  K  R  L  L  T  I  L  S  T

361  TAACTCATCTCCTTTTGGTGATTCAACTGAACGGTTAGTCCATCAATTTACTCGCGCACT  420
      N  S  S  P  F  G  D  S  T  E  R  L  V  H  Q  F  T  R  A  L

421  TTCCCTTCGTCTCAACCGCTATATATCGTCAACCACCAATCATTTCATGACACCTGTTGA  480
      S  L  R  L  N  R  Y  I  S  S  T  T  N  H  F  M  T  P  V  E

481  AACAACTCCAACTGATTCTTCTTCTTCGTCATCATTAGCTCTAATTCAATCATCATATCT  540
      T  T  P  T  D  S  S  S  S  S  S  L  A  L  I  Q  S  S  Y  L

541  ATCTCTAAACCAAGTTACCCCTTTCATAAGGTTTACTCAATTAACCGCTAATCAAGCGAT  600
      S  L  N  Q  V  T  P  F  I  R  F  T  Q  L  T  A  N  Q  A  I

601  TTTAGAAGCGATTAACGGTAATCATCAAGCAATCCACATCGTTGATTTCGACATTAATCA  660
      L  E  A  I  N  G  N  H  Q  A  I  H  I  V  D  F  D  I  N  H

661  CGGGGTTCAATGGCCACCGTTAATGCAAGCACTAGCTGATCGTTACCCTGCTCCCACTCT  720
      G  V  Q  W  P  P  L  M  Q  A  L  A  D  R  Y  P  A  P  T  L

721  TCGAATCACCGGTACTGGAAATGACCTTGATACCCTTCGTAGAACAGGTGATCGTTTAGC  780
      R  I  T  G  T  G  N  D  L  D  T  L  R  R  T  G  D  R  L  A

781  TAAATTTGCTCACTCATTAGGGTTGAGATTTCAATTCCATCCTCTTTATATAGCCAATAA  840
      K  F  A  H  S  L  G  L  R  F  Q  F  H  P  L  Y  I  A  N  N

841  TAACCACGATCACGATGAAGATCCTTCTATTATTTCCTCCATTGTACTACTCCCTGATGA  900
      N  H  D  H  D  E  D  P  S  I  I  S  S  I  V  L  L  P  D  E

901  AACCCTAGCTATCAACTGTGTTTTCTACCTCCACCGCCTTTTAAAAGACCGCGAAAAGTT  960
      T  L  A  I  N  C  V  F  Y  L  H  R  L  L  K  D  R  E  K  L

961  AAGGATTTTTTTTGCATAGGGTTAAGTCAATGAACCCTAAAATTGTTACAATCGCGGAGAA 1020
      R  I  F  L  H  R  V  K  S  M  N  P  K  I  V  T  I  A  E  K

1021 GGAAGCAAATCATAACCATCCTCTTTTTTTACAAAGATTCATCGAGGCGTTGGATTATTA 1080
```

Fig. 5 contd.

```
841  AGGATTTTTTTGCATAGGGTTAAGTCAATGAACCCTAAAATTGTTACAATCGCGGAGAAG   900
281  R  I  F  L  H  R  V  K  S  M  N  P  K  I  V  T  I  A  E  K    300
901  GAAGCAAATCATAACCATCCTCTTTTTTTACAAAGATTTATCGAGGCGTTGGATTATTAT   960
301  E  A  N  H  N  H  P  L  F  L  Q  R  F  I  E  A  L  D  Y  Y    320
961  ACAGCTGTGTTTGATTCATTGGAAGCTACATTGCCACCGGGTAGTCGTGAGAGGATGACA  1020
321  T  A  V  F  D  S  L  E  A  T  L  P  P  G  S  R  E  R  M  T    340
1021 GTTGAACAAGTGTGGTTTGGGAGAGAAATTGTTGATATCGTGGCGATGGAAGGAGATAAA  1080
341  V  E  Q  V  W  F  G  R  E  I  V  D  I  V  A  M  E  G  D  K    360
1081 AGGAAAGAAAGACATGAAAGGTTTAGATCATGGGAAGTTATGTTGAGGAGTTGTGGATTT  1140
361  R  K  E  R  H  E  R  F  R  S  W  E  V  M  L  R  S  C  G  F    380
1141 AGTAATGTTGCTTTAAGCCCTTTTGCATTATCACAAGCTAAGCTTCTTTTGAGACTACAT  1200
381  S  N  V  A  L  S  P  F  A  L  S  Q  A  K  L  L  L  R  L  H    400
1201 TATCCTTCTGAAGGCTATCAACTCGGAGTTTCGAGTAATTCTTTCTTCTTAGGTTGGCAA  1260
401  Y  P  S  E  G  Y  Q  L  G  V  S  S  N  S  F  F  L  G  W  Q    420
1261 AATCAACCTCTTTTCTCCATCTCGTCTTGGCGTTGA  1296
421  N  Q  P  L  F  S  I  S  S  W  R  *    432
```

Fig. 6

```
  1 ATGTTAGGATCCTTTGGTTCTTCATCATCTCAATCTCACCCTCATCATGATGAAGAATCT  60
  1 M  L  G  S  F  G  S  S  S  S  Q  S  H  P  H  H  D  E  E  S   20
 61 TCTGATCATCATCAACGGCGTAGATTCACCGCTACTACTACAACTATCACCACCACCACC 120
 21 S  D  H  H  Q  R  R  R  F  T  A  T  T  T  T  I  T  T  T  T   40
121 ACAACGACCTCACCAGCTATTCAAATCCGCCAGCTACTCATTAGCTGTGCGGAGTTGATT 180
 41 T  T  T  S  P  A  I  Q  I  R  Q  L  L  I  S  C  A  E  L  I   60
181 TCGCGGTCCGATTTCTCGGCCGCGAAAAGACTCCTTACCATATTATCAACTAACTCTTCT 240
 61 S  R  S  D  F  S  A  A  K  R  L  L  T  I  L  S  T  N  S  S   80
241 CCTTTTGGTGATTCAACTGAACGGTTAGTCCATCAGTTTACTCGCGCACTTTCCCTTCGT 300
 81 P  F  G  D  S  T  E  R  L  V  H  Q  F  T  R  A  L  S  L  R  100
301 CTCAACCGCTATATATCGTCAACCACCAATCATTTCATGACACCTGTTGAAACAACTCCA 360
101 L  N  R  Y  I  S  S  T  T  N  H  F  M  T  P  V  E  T  T  P  120
361 ACTGATTCTTCATCTTCGTTGCCATCGTCATCATTAGCTCTAATTCAATCATCATATCAT 420
121 T  D  S  S  S  S  L  P  S  S  S  L  A  L  I  Q  S  S  Y  H  140
421 TCTCTAAATCAAGTTACCCCTTTTATAAGGTTTACTCAATTAACCGCTAATCAAGCGATT 480
141 S  L  N  Q  V  T  P  F  I  R  F  T  Q  L  T  A  N  Q  A  I  160
481 TTAGAAGCGATTAACGGTAATCATCAAGCAATCCACATCGTTGATTTCGACATTAATCAC 540
161 L  E  A  I  N  G  N  H  Q  A  I  H  I  V  D  F  D  I  N  H  180
541 GGGGTTCAATGGCCACCGTTAATGCAAGCACTAGCTGATCGTTACCCTGCTCCTACTCTT 600
181 G  V  Q  W  P  P  L  M  Q  A  L  A  D  R  Y  P  A  P  T  L  200
601 CGAATCACCGGTACTGGAAATGACCTTGATACCCTTCGTAGAACAGGTGATCGTTTAGCT 660
201 R  I  T  G  T  G  N  D  L  D  T  L  R  R  T  G  D  R  L  A  220
661 AAATTTGCTCACTCATTAGGGTTGAGATTTCAATTCCATCCTCTTTATATCGCCAATAAT 720
221 K  F  A  H  S  L  G  L  R  F  Q  F  H  P  L  Y  I  A  N  N  240
721 AACCGCGATCACGGTGAAGATCCTTCTATTATTTCCTCCATTGTACTTCTCCCTGATGAA 780
241 N  R  D  H  G  E  D  P  S  I  I  S  S  I  V  L  L  P  D  E  260
781 ACCCTAGCTATCAACTGTGTTTTCTATCTCCACCGCCTTTTAAAAGACCGCGAAAAATTA 840
261 T  L  A  I  N  C  V  F  Y  L  H  R  L  L  K  D  R  E  K  L  280
```

Fig. 6 contd.

```
1   GAGAGGTCATCAAACCCTAGCAGTCCACCTCCATCTCTCCGCATAACCGGATGCGGTCGA   60
    E  R  S  S  N  P  S  S  P  P  P  S  L  R  I  T  G  C  G  R
61  GATGTAACCGGATTAAACCGAACTGGAGACCGGTTAACCCGGTTCGCTGACTCTTTAGGT  120
    D  V  T  G  L  N  R  T  G  D  R  L  T  R  F  A  D  S  L  G
121 CTCCAATTCCAGTTTCACACGCTAGTGATCGTAGAAGAAGATCTCGCCGGACTTTTGCTA  180
    L  Q  F  Q  F  H  T  L  V  I  V  E  E  D  L  A  G  L  L  L
181 CAGATCCGATTGTTAGCTCTCTCAGCCGTACAAGGAGAGACCATTGCCGTCAATTGTGTT  240
    Q  I  R  L  L  A  L  S  A  V  Q  G  E  T  I  A  V  N  C  V
241 CACTTCCTCCACAAAATATTTAACGACGATGGAGATATGATCGGTCACTTCTTGTCAGCG  300
    H  F  L  H  K  I  F  N  D  D  G  D  M  I  G  H  F  L  S  A
301 ATCAAGAGCTTAAACTCTAGAATCGTTACAATGGCAGAGAGAGAAGCTAATCATGGAGAT  360
    I  K  S  L  N  S  R  I  V  T  M  A  E  R  E  A  N  H  G  D
361 CACTCGTTCTTGAATAGATTCTCTGAGGCAGTGGATCATTACATGGCGATCTTTGATTCG  420
    H  S  F  L  N  R  F  S  E  A  V  D  H  Y  M  A  I  F  D  S
421 TTGGAAGCGACGTTGCCGCCAAATAGCCGAGAGAGACTAACCCTAGAGCAACGGTGGTTC  480
    L  E  A  T  L  P  P  N  S  R  E  R  L  T  L  E  Q  R  W  F
481 GGTAAGGAGATTTTGGATGTTGTGGCGGCGGAAGAGACGGAGAGAAAGCAAAGACATCGG  540
    G  K  E  I  L  D  V  V  A  A  E  E  T  E  R  K  Q  R  H  R
541 AGGTTTGAGATTTGGGAAGAGATGATGAAGAGGTTTGGTTTCGTTAACGTTCCTATTGGA  600
    R  F  E  I  W  E  E  M  M  K  R  F  G  F  V  N  V  P  I  G
601 AGCTTTGCTTTGTCTCAAGCTAAGCTTCTTCTTAGACTTCATTATCCTTCAGAAGGTTAT  660
    S  F  A  L  S  Q  A  K  L  L  L  R  L  H  Y  P  S  E  G  Y
661 AATCTTCAGTTCCTTAACAATTCTTTG  687
    N  L  Q  F  L  N  N  S  L
```

Fig. 7

```
LsAt    1  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
LsLe    1  MLGSFGSSSSQSHPHHDEESSDHHQQRRFTATATTITTTTLTTSPAIQIRQLLISCAELI
LsSt    1  MLGSFGSSSSQSHPHHDEESSDHHQRRRFTATTTTITTTTTTTSPAIQIRQLLISCAELI

LsAt    1  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
LsLe   61  SQSDFSAAKRLLTILSTNSSPFGDSTERLVHQFTRALSLRLNRYISSTTNHFMTPVETTP
LsSt   61  SRSDFSAAKRLLTILSTNSSPFGDSTERLVHQFTRALSLRLNRYISSTTNHFMTPVETTP

LsAt    1  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
LsLe  121  TDSSS...SSSLALIQSSYLSLNQVTPFIRFTQLTANQAILEAINGNHQAIHIVDFDINH
LsSt  121  TDSSSSLPSSSLALIQSSYHSLNQVTPFIRFTQLTANQAILEAINGNHQAIHIVDFDINH

LsAt    1  ~~~~~~~ERSSNPSSPPPSLRITGCGRDVTGLNRTGDRLTRFADSLGLQFQFHTLVIVEE
LsLe  178  GVQWPPLMQALADRYPAPTLRITGTGNDLDTLRRTGDRLAKFAHSLGLRFQFHPLYIANN
LsSt  181  GVQWPPLMQALADRYPAPTLRITGTGNDLDTLRRTGDRLAKFAHSLGLRFQFHPLYIANN

LsAt   54  DLAGLLLQIRELALSAVQGETLAINCVHFLHKIFNDDGDMIGHFLSAIKSLNSRIVTIAE
LsLe  238  NHDHDEDPSIISSIVLLPDETLAINCVFYLHRLLK.DREKLRIFLHRVKSMNPKIVTIAE
LsSt  241  NRDHGEDPSIISSIVLLPDETLAINCVFYLHRLLK.DREKLRIFLHRVKSMNPKIVTIAE

LsAt  114  REANHGDHSFLNRFSEAVDHVMAEFDSLEATLPPNSRERITLEQRVFGKEILDLVAAEET
LsLe  297  KEANHNHPLFLQRFIEALDYYTAVFDSLEATLPPGSRERMTVEQVWFGREIVDIVAMEGD
LsSt  300  KEANHNHPLFLQRFIEALDYYTAVFDSLEATLPPGSRERMTVEQVWFGREIVDIVAMEGD

LsAt  174  ERKERHRRFEIVEENMKRFGFVNVPLGSFALSQAKLLLRLHYPSEGYLLQFLNNSL~~~~
LsLe  357  KRKERHERFRSWEVMLRSCGFSNVALSPFALSQAKLLLRLHYPSEGYQLGVSSNSFFLGW
LsSt  360  KRKERHERFRSWEVMLRSCGFSNVALSPFALSQAKLLLRLHYPSEGYQLGVSSNSFFLGW

LsAt  230  ~~~~~~~~~~~~~~
LsLe  417  QNQPLFSISSWR
LsSt  420  QNQPLFSISSWR
```

Fig. 8